

7. (Amended) The method of claim 1 wherein said sequence-specific tag is chosen from one or more of the group consisting of a nucleic acid, a protein, and a single molecule conjugated to a microparticle or a nanoparticle.

9. (Amended) The method of claim 1 wherein the nucleic acid sample is DNA chosen from one or more of the group consisting of a cosmid, a bacterial artificial chromosome, and a yeast artificial chromosome.

16. (Amended) The method of claim 15 wherein the functional group is chosen from one or more of the group consisting of biotin-avidin complexes, primary amines, sulfhydryl groups, single stranded binding proteins, and histidine terminated oligonucleotides.

17. (Amended) The method of claim 16 wherein the deposition surface is a on dipstick.

18. (Amended) The method of claim 17 wherein the deposition surface on the dipstick has specific areas for tethering different types of function group modified nucleic acid sequences.

Please add the following new claims:

32 (New) A method for analyzing a nucleic acid sample comprising:

- (a) obtaining a nucleic acid sample by cutting and linearizing a strand of nucleic acid;
- (b) preparing a surface;
- (c) tethering the linearized nucleic acid sample to the surface;
- (d) tagging two or more sequence specific sites of the tethered nucleic acid sample

with a sequence specific tag;

- (e) drying the nucleic acid sample;
- (f) scanning the nucleic acid sample with a scanning probe microscope; and
- (g) analyzing the scan to determine the distance between the tagged nucleic acid sites.

33. (New) The method of claim 32 wherein preparing the surface further comprises modifying the surface with an alkanethiolate.
34. (New) The method of claim 32 wherein tethering the linearized nucleic acid sample to the surface further comprises modifying one or both ends of the nucleic acid sample with a reactive group that will react with the prepared surface.
35. (New) The method of claim 32 wherein scanning the nucleic acid sample further comprises bleeding a low moisture inert gas over the tethered nucleic acid sample.
36. (New) The method of claim 32 wherein analyzing the scan further comprises forming bar code readouts wherein the bars represent a tagged nucleic acid sample and the distance between the bars represents the distance between the tagged sequence specific sites.
37. (New) The method of claim 12 further comprising tethering the nucleic acid sample to a deposition surface
38. (New) The method of claim 37 wherein the deposition surface is on a dipstick.
39. (New) The method of claim 28 wherein the deposition surface on the dipstick has specific areas for tethering different types of nucleic acid sequences.
40. (New) A method for analyzing a nucleic acid sample, the method comprising
- (a) tagging one or more sequence specific sites of the nucleic acid;
  - (b) scanning the nucleic acid sample; and
  - (c) analyzing the scan of the nucleic acid sample to determine the distance between the one or more tagged nucleic acid sequences and the end of the nucleic acid sequence.